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UniProtKB/TrEMBL entry

Q0PBL7

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Entry information

Entry name	Q0PBL7_CAMJE
Primary accession number	Q0PBL7
Secondary accession numbers	None
Integrated into TrEMBL on	September 19, 2006
Sequence was last modified on	September 19, 2006 (Sequence version 1)
Annotations were last modified on	July 22, 2008 (Entry version 13)
Name and origin of the protein	
Protein name	Major antigenic peptide PEB3 [Precursor]
Synonyms	None
Gene name	Name: <i>peb3</i> OrderedLocusNames: <i>Cj0289c</i>
From	<i>Campylobacter jejuni</i> [TaxID: 197] [HAMAP proteome]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobact
Protein existence	1: Evidence at protein level;

References

- [1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 STRAIN=NCTC 11168 / Serotype O:2;
 DOI=10.1038/35001088; PubMed=10688204 [NCBI, ExPASy, EBI, Israel, Japan]
 Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M., Basham D., Chillingworth
 Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Per
 C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Ba

B.G.;

"The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hypervariable sequences.";

Nature 403:665-668(2000).

Comments

- INTERACTION:**

Q0PBH3:motB; NbExp=1; IntAct=EBI-1192366, EBI-1191146;

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Cross-references

Sequence databases

EMBL	AL111168; CAL34442.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
PIR	G81447; G81447.	

3D structure databases

PDB	2HXW; X-ray; 1.60 A; A/B=21-250.[ExpASy / RCSB / EBI]
PDBsum	2HXW; -.
ModBase	Q0PBL7.

Protein-protein interaction databases

IntAct	Q0PBL7; -.
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Ontologies

GO	GO:0005515; Molecular function: protein binding (<i>inferred from physical interaction from IntAct</i>).
	QuickGo view.

Genome annotation databases

GenomeReviews	AL111168_GR; Cj0289c.
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KEGG	cje:Cj0289c; -.
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Phylogenomic databases

HOGENOM	Q0PBL7; -.
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Genome annotation databases

CMR	Q0PBL7; Cj0289c.
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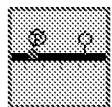
Other

UniRef	View cluster of proteins with at least 50% / 90% / 100% identity.
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Keywords

Complete proteome; Signal.

Features



Feature table viewer

Key	From	To	Length	Description	FTId
SIGNAL	1	20	20	Potential.	

CHAIN 21 250 230 Potential. PRO_5000074997

Sequence information

Length: 250 AA [This is the length of the unprocessed precursor] Molecular weight: 27537 Da [This is the MW of the unprocessed precursor] CRC64: B2A9AF0630A04065 is a checksum on the sequence

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      10      20      30      40      50      60
MKKIITLFGA CALAFSMANA DVNLYGPGGP HTALKDIANK YSEKTGVKVN VNFQATWF
      70      80      90     100     110     120
EKAKKDADIL FGASDQSALA IASDFGKDFN VSKIKPLYFR EAIILTQKGN PLKIKGLKDL
     130     140     150     160     170     180
ANKKVRIVVP EGAGKSNSTG TGVWEDMIGR TQDIKTIQNF RNNIVAFVPN SGSARKLFAQ
     190     200     210     220     230     240
DQADAWITWI DWSKSNPDIG TAVAIEKDLV VYRTFNVIK EGASKETQDF IAYLSSKEAK
     250
EIFKKYGWRE

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BLAST

BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam,
ProtScale, Compute pI/Mw, PeptideMass,
PeptideCutter, Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to
SWISS-MODEL



NPSA Sequence
analysis tools



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